

SEQUENCE LISTING

<110> WINDSOR-HINES, Dawn
 RAO, Patricia
 RINGLER, Douglas J.

<120> INDUCING TOLERANCE IN PRIMATES

<130> TLN-022

<150> 60/431839

<151> 2002-12-09

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(717)

<400> 1

atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
 35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
 65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys

100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
225 230 235

<210> 2
<211> 716
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 2
atggagacag acacaatcct gctatgggtg ctgctgctct ggggtccagg ctccactggt 60
gacattgtga tgaccaatc tccagattct ttgctgtgt ctctaggtga gagggccacc 120
atcaactgca aggccagcca aagtgttgat tatgatgggtg atagttatat gaactggtat 180
caacagaaac caggacagcc acccaaactc ctcattctatg ttgcatccaa tctagagtct 240
gggtgccag acaggttag tggcagtggg tctgggacag acttcaccct caccatcagt 300
tctctgcagg cggaggatgt tgcagtctat tactgtcagc aaagtcttca ggaccctccg 360
acgttcggtg gaggtaccaa ggtggaaatc aaacgaactg tggctgcacc atctgtcttc 420
atctcccg ccatctgatga gcagtigaaa tctggaactg cctctgttgt gtgcctgctg 480
aataacttct atccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 540
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600
acaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcgaagtca 660

cccatcaggg cctgagctcg cccgtcaca agagcttcaa caggggagag tgtag 716

<210> 3

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 3

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
 35 40 45
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
 65 70 75 80
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95
 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
 100 105 110
 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 115 120 125
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 180 185 190
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 4

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 4

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
 85 90 95
 Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 5
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<221> CDS
 <222> (1)...(1404)

<400> 5
 atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
 Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
 1 5 10 15
 gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn

65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc gcg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
245 250 255

gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

| | | | |
|--|-----|-----|-----|
| 290 | 295 | 300 | |
| cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 960 | | | |
| His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr | | | |
| 305 | 310 | 315 | 320 |
| cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008 | | | |
| Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly | | | |
| 325 | 330 | 335 | |
| aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056 | | | |
| Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile | | | |
| 340 | 345 | 350 | |
| gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104 | | | |
| Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val | | | |
| 355 | 360 | 365 | |
| tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152 | | | |
| Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser | | | |
| 370 | 375 | 380 | |
| ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200 | | | |
| Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu | | | |
| 385 | 390 | 395 | 400 |
| tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248 | | | |
| Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro | | | |
| 405 | 410 | 415 | |
| gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296 | | | |
| Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val | | | |
| 420 | 425 | 430 | |
| gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344 | | | |
| Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met | | | |
| 435 | 440 | 445 | |
| cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1392 | | | |
| His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser | | | |
| 450 | 455 | 460 | |
| ccg ggt aaa tga 1404 | | | |
| Pro Gly Lys * | | | |
| 465 | | | |

<210> 6
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Chimeric Sequence

 <400> 6

atggaatgga tctggatctt tctcctcatc ctgtcaggaa ctgaggtgt ccagtcaccag 60
gttcagctgg tgcagtctgg agctgaagtg aagaagcctg gggcttcagt gaagtggtcc 120
tgtaaggctt ctggatacac attcactgcc tatgtataa gctgggtgag gcaggcacct 180
ggacagggcc ttgagtggat gggagagatt tatcctggaa gcggtagtag ttattataat 240
gagaagtca agggcagggt cacaatgact agagacacat ccaccagcac agtctacatg 300
gaactcagca gcctgaggtc tgaggacact gcggtctatt actgtgcaag atccggggac 360
ggcagtcggt ttgttactg gggccaaggg acactagtca cagtctcctc agcctccacc 420
aaggggccat cgggtctccc cctggcaccc tctccaaga gcacctctgg gggcacagcg 480
gccttgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca 540
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtctc aggactctac 600
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatctgt 720
gacaaaactc acatagccc accgtgcccga gcacctgaac tcgcgggggc accgtcagtc 780
ttctcttccc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
tgctgtggtg tgacgtgag ccacgaagac cctgaggtca agtcaactg gtacgtggac 900
ggcgtggagg tgataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 960
cgtgtgtgca gcgtctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaaggtct ccaacaaagc cctcccagcc ccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1140
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 1260
gacggctcct tcttctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320
aacgtcttct catgtccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
ctctccctgt ctccgggtaa atga 1404

<210> 7

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 7

Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
245 250 255
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460
Pro Gly Lys
465

<210> 8

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 8

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe

50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 9

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(717)

<400> 9

atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cta tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220

ctg agc tgc ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
 225 230 235

<210> 10
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 10
 atggagacag acacaatcct gctatgggtg ctgctgctct gggttccagg ctccactggt 60
 gacattgtga tgacccaatc tccagattct ttggctgtgt ctctaggtga gagggccacc 120
 atcaactgca aggccagcca aagtgtgat tatgatgggt atagtatat gaactggtat 180
 caacagaaac caggacagcc acccaaactc ctcatctatg ttgcaccaa tctagagtct 240
 ggggtcccag acaggttttag tggcagtggg tctgggacag acttcaccct caccatcagt 300
 tctctgcagg cggaggatgt tgcagtctat tactgtcagc aaagtcttca ggacctccg 360
 acgttcggtg gaggtaccaa ggtggaaatc aaacgaactg tggctgcact atctgtctc 420
 atctccgcgc catctgatga gcagtgaaa tctggaactg cctctgttgt gtgcctgctg 480
 aataactct atcccagaga ggccaaagta cagtggagg tggataacgc cctccaatcg 540
 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600
 agcaccctga cgctgagcaa agcagactac gagaacaca aagtctacgc ctgcgaagtc 660
 acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgtag 717

<210> 11
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 11
 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
 35 40 45
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
 65 70 75 80
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
 100 105 110
 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 115 120 125
 Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
 130 135 140
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 180 185 190
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 12
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 12
 Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
 85 90 95
 Gln Asp Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 13

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(1404)

<400> 13

atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48

Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly

1 5 10 15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96

Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

20 25 30

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192

Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240

Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn

65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288

Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser

85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384

Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly

115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala

145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

tgc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac gcc agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccg ggt aaa tga 1404
Pro Gly Lys *
465

<210> 14
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 14
atggaatgga tctggtctt tctctcatc ctgtcaggaa ctgaggtgt ccagtcacag 60
gttcagctgg tgcagtctgg agctgaagtg aagaagcctg gggcttcagt gaaggtgtcc 120
tgtaaggctt ctggatacac attcactgcc tatgttataa gctgggtgag gcaggcacct 180
ggacagggcc ttgagtggat gggagagatt tctctggaa gcggtagtag ttattataat 240
gagaagtta agggcagggt cacaatgact agagacacat ccaccagcac agtctacatg 300
gaactcagca gcctgaggtc tgaaggacact gcggtctatt actgtgcaag atccggggac 360
ggcagtcggt ttgttactg gggccaaggg acactagtca cagtctctc agcctccacc 420
aagggcccat cggcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480
gccctgggct gcctgtgcaa ggactactc cccgaaccgg tgacggtgtc gtggaactca 540
ggcgccctga ccagcggcgt gcacacctc ccggctgtcc tacagtctc aggactctac 600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
gacaaaactc acacatgccc accgtgccc gcacctgaac tctgggggg accgtcagtc 780
ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc taggtcaca 840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agtcaactg gtacgtggac 900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtagcg cagcacgtac 960
cgtgtggtca gcgtctcac cgtctgcac caggactggc tgaatggcaa ggagtacaag 1020
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1140
aaccaggtca gcctgacctg cctgtgcaaa ggcttctatc ccagcgacat cgccgtggag 1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 1260
gacggctctt tcttctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320
aacgtcttct catgctcgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380

ctctccctgt ctccgggtaa atga

1404

<210> 15

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 15

Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
1 5 10 15
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
305 310 315 320
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys
 465

<210> 16
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 16
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
 20 25 30
 Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 17

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(717)

<400> 17

atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro
1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96

Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
115 120 125

gaa atc aaa cga act gtg gct gca cta tct gtc ttc atc ttc ccg cca 432
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
225 230 235

<210> 18
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric Sequence

<400> 18

atggagacag acacaatcct gctatgggtg ctgctgctct gggttccagg ctccactggt 60
gacattgtga tgaccaatc tccagattct ttggctgtgt ctctaggtga gagggccacc 120
atcaactgca aggccagcca aagtgtgat tatgatggtg atagttatat gaactggtat 180
caacagaaac caggacagcc acccaaactc ctcatctatg ttgcatcaa tctagagtct 240
gggtgtccag acaggttttag tggcagtggg tctgggacag acttcaccct caccatcagt 300
tctctgcagg cggaggatgt tgcagtctat tactgtcagc aaagtcttca ggaccctccg 360
acgttcggtg gaggtaccaa ggtggaaatc aaacgaactg tggctgcact atctgtcttc 420
atcttccgc catctgatga gcagtgaaa tctggaactg cctctgttgt gtgcctgctg 480
aataacttct atccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 540
ggttaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600
agcacctga cgctgagcaa agcagactac gagaacaca aagtctacgc ctgcgaagtc 660
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgtag 717

<210> 19

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 19

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
35 40 45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
65 70 75 80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
100 105 110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
115 120 125
Glu Ile Lys Arg Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro
130 135 140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 20

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 20

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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1      5      10     15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20     25     30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35     40     45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
 50     55     60
Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65     70     75     80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
 85     90     95
Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100    105    110
Thr Val Ala Ala Leu Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115    120    125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130    135    140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145    150    155    160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165    170    175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180    185    190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195    200    205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210    215

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<210> 21

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(1404)

<400> 21

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atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
 1      5      10     15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20     25     30

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cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
115 120 125

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc gcg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
245 250 255

gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccg ggt aaa tga 1404
Pro Gly Lys *
465

<210> 22
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 22
 atggaatgga tctgcatctt tctctcacc ctgtcaggaa ctgaggtgt ccagtcccag 60
 gttcagctgg tgcagctctg agctgaagtg aagaagcctg gggcttcagt gaaggtgtcc 120
 tgaaggctt ctgatacac attcactgcc tatgtataa gctgggtgag gcaggcacct 180
 ggacagggcc ttgagtggat gggagagatt tctctggaa gcggtagtag ttattataat 240
 gagaagtta agggcagggt cacaatgact agagacacat ccaccagcac agtctacatg 300
 gaactcagca gcctgaggtc tgaaggacact gcggtctatt actgtgcaag atccggggac 360
 ggagctcgtt ttgttactg gggccaaggg acactagtca cagtctctc agcctccacc 420
 aaggggccat cgggttccc ctggcacc cctccaaga gcacctctgg gggcacagcg 480
 gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540
 ggcgccctga ccagcggcgt gcacaccttc ccggtgttcc tacagtctc aggactctac 600
 tccctcagca gcgtggtgac cgtgccttcc agcagcttgg gcaccagac ctacatctgc 660
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720
 gacaaaactc acacatgccc accgtgccc gcacctgaac tcgcgggggc accgtcagtc 780
 ttccttctcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
 tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agtcaactg gtacgtggac 900
 ggctgtggag tgcatatgc caagacaaag ccgctggagg agcagtaca cagcacgtac 960
 cgtgtggtca gcctctcac cgtctgcac caggactggc tgaatggcaa ggagtacaag 1020
 tgaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080
 gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1140
 aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
 tgggagagca atgggcagcc ggagaacaac tacaagacca gcctcccgt gctggactcc 1260
 gacggctcct tcttctcta cagcaagctc accgtggaca agagcagggt gcagcagggg 1320
 aacgttctct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
 ctctccctgt ctccgggtaa atga 1404

<210> 23
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 23
 Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
 1 5 10 15
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser

85 90 95
 Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
 115 120 125
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 210 215 220
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 225 230 235 240
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly
 245 250 255
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 275 280 285
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys
 465

<210> 24

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 24

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30
Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser
225 230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 25
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<221> CDS
 <222> (1)...(717)

<400> 25
 atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca 48
 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

ggc tcc act ggt gac att gtg atg acc caa tct cca gat tct ttg gct 96
 Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tct cta ggt gag agg gcc acc atc aac tgc aag gcc agc caa agt 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
 35 40 45

gtt gat tat gat ggt gat agt tat atg aac tgg tat caa cag aaa cca 192
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60

gga cag cca ccc aaa ctc ctc atc tat gtt gca tcc aat cta gag tct 240
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
 65 70 75 80

ggg gtc cca gac agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

ctc acc atc agt tct ctg cag gcg gag gat gtt gca gtc tat tac tgt 336
 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
 100 105 110

cag caa agt ctt cag gac cct ccg acg ttc ggt gga ggt acc aag gtg 384
 Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
 115 120 125

gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca 432
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140

tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg 480
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu

145 150 155 160

aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac 528
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175

gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc 576
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 180 185 190

aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca 624
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205

gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag gcc 672
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220

ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 717
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
 225 230 235

<210> 26
 <211> 716
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 26
 atggagacag acacaatcct gctatgggtg ctgctgctct gggttccagg ctccactggt 60
 gacattgtga tgaccaatc tccagattct ttggctgtgt ctctaggtga gagggccacc 120
 atcaactgca aggccagcca aagtgttgat tatgatggtg atagtatat gaactggtat 180
 caacagaaac caggacagcc acccaaactc ctcatctatg ttgcaccaa tctagagtct 240
 ggggtcccg acaggtttag tggcagtggg tctgggacag acttcacct caccatcagt 300
 tctctgcagg cggaggatgt tgcagtctat tactgtcagc aaagtctca ggacctccg 360
 acgttcggtg gaggtacca ggtggaaatc aaacgaactg tggctgcacc atctgtctc 420
 atctcccg ccatctgatga gcagttgaaa tctggaactg cctctgtgtg gtgcctgctg 480
 aataacttct atccagaga ggccaaagta cagtggaaagg tggataacgc cctccaatcg 540
 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600
 acacctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcgaagtca 660
 cccatcaggg cctgagctcg cccgtcaca agagcttcaa caggggagag tggttag 716

<210> 27
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 27
 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro

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1      5      10      15
Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
      20      25      30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser
      35      40      45
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
      50      55      60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser
      65      70      75      80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
      85      90      95
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
      100     105     110
Gln Gln Ser Leu Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
      115     120     125
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
      130     135     140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
      145     150     155     160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
      165     170     175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
      180     185     190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
      195     200     205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
      210     215     220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      225     230     235

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<210> 28

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 28

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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1      5      10      15
Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
      20      25      30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
      35      40      45
Lys Leu Leu Ile Tyr Val Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
      50      55      60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
      65      70      75      80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Leu
      85      90      95
Gln Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
      100     105     110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
      115     120     125

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Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 29

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(1404)

<400> 29

atg gaa tgg atc tgg atc ttt ctc ctc atc ctg tca gga act cga ggt 48
 Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
 1 5 10 15

gtc cag tcc cag gtt cag ctg gtg cag tct gga gct gaa gtg aag aag 96
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

cct ggg gct tca gtg aag gtg tcc tgt aag gct tct gga tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

act gcc tat gtt ata agc tgg gtg agg cag gca cct gga cag ggc ctt 192
 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

gag tgg atg gga gag att tat cct gga agc ggt agt agt tat tat aat 240
 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
 65 70 75 80

gag aag ttc aag ggc agg gtc aca atg act aga gac aca tcc acc agc 288
 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
 85 90 95

aca gtc tac atg gaa ctc agc agc ctg agg tct gag gac act gcg gtc 336
 Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

tat tac tgt gca aga tcc ggg gac ggc agt cgg ttt gtt tac tgg ggc 384
 Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly

| | | | |
|--|-----|-----|-----|
| 115 | 120 | 125 | |
| caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg 432 | | | |
| Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser | | | |
| 130 | 135 | 140 | |
| gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 480 | | | |
| Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala | | | |
| 145 | 150 | 155 | 160 |
| gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 528 | | | |
| Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val | | | |
| 165 | 170 | 175 | |
| tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 576 | | | |
| Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala | | | |
| 180 | 185 | 190 | |
| gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624 | | | |
| Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val | | | |
| 195 | 200 | 205 | |
| ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672 | | | |
| Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His | | | |
| 210 | 215 | 220 | |
| aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 720 | | | |
| Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys | | | |
| 225 | 230 | 235 | 240 |
| gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 768 | | | |
| Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly | | | |
| 245 | 250 | 255 | |
| gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816 | | | |
| Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met | | | |
| 260 | 265 | 270 | |
| atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864 | | | |
| Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His | | | |
| 275 | 280 | 285 | |
| gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912 | | | |
| Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val | | | |
| 290 | 295 | 300 | |
| cat aat gcc aag aca aag ccg cgg gag gag cag tac gcc agc acg tac 960 | | | |
| His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr | | | |
| 305 | 310 | 315 | 320 |
| cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008 | | | |
| Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly | | | |
| 325 | 330 | 335 | |
| aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056 | | | |
| Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile | | | |

| | | | |
|--|-----|------|-----|
| 340 | 345 | 350 | |
| gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1104 | | | |
| Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val | | | |
| 355 | 360 | 365 | |
| tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1152 | | | |
| Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser | | | |
| 370 | 375 | 380 | |
| ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200 | | | |
| Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu | | | |
| 385 | 390 | 395 | 400 |
| tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1248 | | | |
| Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro | | | |
| 405 | 410 | 415 | |
| gtg ctg gac tcc gac ggc tcc ttc ttc ctg tac agc aag ctg acc gtg 1296 | | | |
| Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val | | | |
| 420 | 425 | 430 | |
| gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1344 | | | |
| Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met | | | |
| 435 | 440 | 445 | |
| cat gag gct ctg cac aac cac tac acg cag aag agc ctg tcc ctg tct 1392 | | | |
| His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser | | | |
| 450 | 455 | 460 | |
| ccg ggt aaa tga | | 1404 | |
| Pro Gly Lys * | | | |
| 465 | | | |

<210> 30
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<400> 30
 atggaatgga tctggatctt tctcctcacc ctgtcaggaa ctgaggtgt ccagtcccag 60
 gttcagctgg tgcagtctgg agctgaagtg aagaagcctg gggcttcagt gaaggtgtcc 120
 tgtaaggctt ctggatacac attcactgcc tatgttataa gctgggtgag gcaggcacct 180
 ggacagggcc ttgagtggat gggagagatt tctcctggaa gcggtagtag ttattataat 240
 gagaagtcca agggcagggt cacaatgact agagacacat ccaccagcac agtctacatg 300
 gaactcagca gcctgaggtc tgaggacact gcggtctatt actgtgcaag atccggggac 360
 ggcagtcggt ttgtttactg gggccaaggg acactagtca cagtctctc agcctccacc 420
 aaggggccat cggcttcccc cctggcacc cctccaaga gcacctctgg gggcacagcg 480
 gccctgggct gcctggtcaa ggactactc cccgaaccgg tgacggtgtc gtggaactca 540
 ggcgccctga ccagcggcgt gcacacctc ccggctgtcc tacagtcctc aggactctac 600
 tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720

gacaaaactc acacatgccc accgtgcccc gcacctgaac tctgggggg accgtcagtc 780
 ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840
 tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 900
 ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacgc cagcacgtac 960
 cgtgtgggtca gctcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020
 tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaacctctc caaagccaaa 1080
 gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1140
 aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1260
 gacggctctt tcttctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1320
 aacgtcttct catgtccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380
 ctctccctgt ctccgggtaa atga 1404

<210> 31

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 31

Met Glu Trp Ile Trp Ile Phe Leu Leu Ile Leu Ser Gly Thr Arg Gly
 1 5 10 15
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ala Tyr Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn
 65 70 75 80
 Glu Lys Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
 85 90 95
 Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly
 115 120 125
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 210 215 220
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 225 230 235 240
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 275 280 285
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460
 Pro Gly Lys
 465

<210> 32

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<400> 32

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
 20 25 30
 Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ser Tyr Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gly Asp Gly Ser Arg Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 33

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric Sequence

<221> CDS

<222> (1)...(1356)

<400> 33

cag gtt caa ttg gtg gag tct gga gga ggc gtt gta cag cct gga agg 48
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

tcc ctg aga ctc tca tgt gca gct tct gga ttc act ttc agt gac ttt 96

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

ggc atg aac tgg gtt cga cag gct ccc ggg aag ggg ctg gaa tgg gtg 144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca ctg att tac tat gat ggt agt aac aag ttc tat gca gac tct gtg 192
Ala Leu Ile Tyr Tyr Asp Gly Ser Asn Lys Phe Tyr Ala Asp Ser Val
50 55 60

aag ggt cga ttc acc atc tcc agg gac aat tct aag aac acc cta tac 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aaa ccc cac tat gat ggt tat tat cac ttc ttt gat tcc tgg ggc 336
Ala Lys Pro His Tyr Asp Gly Tyr Tyr His Phe Phe Asp Ser Trp Gly
100 105 110

caa ggg aca cta gtc aca gtc tcc tca gcc tcc acc aag ggc cca tgg 384
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 432
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

tgg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct 528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 624
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt 672
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg 720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 768

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 816
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 864
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 912
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 960
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1008
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 1056
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 1104
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1152
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 1200
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1248
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 1296
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 1344
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

ccg ggt aaa tga 1356
 Pro Gly Lys *
 450

<210> 34
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric Sequence

<221> CDS
 <222> (1)...(642)

<400> 34
 gac atc cag atg acc cag agc cca agc agc ctg agc gcc agc gtg ggt 48
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

gac aga gtg acc atc acc tgt aaa gga agt cag gat att aac aat tac 96
 Asp Arg Val Thr Ile Thr Cys Lys Gly Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

tta gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc 144
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

tac aat aca gac att ttg cac acg ggt gtg cca agc aga ttc agc ggt 192
 Tyr Asn Thr Asp Ile Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca 240
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

gag gac atc gcc acc tac tac tgc tat cag tat aac aac ggg tac acg 288
 Glu Asp Ile Ala Thr Tyr Tyr Cys Tyr Gln Tyr Asn Asn Gly Tyr Thr
 85 90 95

ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca cca 336
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act 384
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa 432
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag 480
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc 528
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc 576
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

tgc gaa gtc acc cat cag ggc ctg agc tgc ccc gtc aca aag agc ttc 624
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

aac agg gga gag tgt tag 642
 Asn Arg Gly Glu Cys *
 210

<210> 35
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 35
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45
 Leu Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Met Phe Gly Gln Gly Thr
 115 120 125
 Lys Val Glu Ile Lys Arg Thr
 130 135

<210> 36
 <211> 142
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 36
 Leu Leu Ala Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln
 1 5 10 15
 Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
 20 25 30
 Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Tyr Met His Trp Val Arg

35 40 45
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser
 50 55 60
 Gly Asn Ser Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met
 65 70 75 80
 Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu
 85 90 95
 Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Lys Leu Ala
 100 105 110
 Thr Thr Ile Phe Gly Val Leu Ile Ile Thr Gly Met Asp Tyr Trp Gly
 115 120 125
 Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
 130 135 140

<210> 37

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 37

tgacattgtg atgacccaat ctccagattc ttggctgtg tctctagggtg agagggccac 60
 catcaactgc aaggcc 76

<210> 38

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 38

tgaactggta tcaacagaaa ccaggacag 29

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 39

agagtctggg gtcccagaca ggttagt 28

<210> 40

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 40
gtcttcagga ccctccgacg ttcggtggag gtaccaagct gg 42

<210> 41
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 41
cacctcacc atcagttctc tgcaggcgga ggatgttgca gtctattagt gt 52

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 42
agctttacag ttactgagca caca 24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 43
tcgatgtgtg ctcaagtaact gtaa 24

<210> 44
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 44
ggttcagctg gtgcagctg gagctgaagt gaagaagcct ggggcttcag tgaaggtgtc 60
ctgtaaggct tctgg 75

<210> 45
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 45
agctgggtga ggcaggcacc tggacagggc cttgagtga tgggagagat tt 52

<210> 46
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 46
caagggcagg gtcacaatga ctagagacac atccaccagc acagtctaca tggaactcag 60

<210> 47
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 47
cagcctgagg tctgaggaca ctgcggtcta ttactgtgca aga 43

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 48
gccaaaggac actagtact gtgt 24

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 49
actctaacca tggaatggat ctggatcttt ctctcatc 39

<210> 50
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 50
tcactgccta tgtataagc tgggtgaggc aggcacctg 39

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 51
actagtcaca gtctcctcag c 21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 52
gaattcattt acccggagac ag 22

<210> 53
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 53
ccgtgcccag cacctgaact cgcgggggca cegtcagtct tctctcccc 49

<210> 54
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 54
ggtaccaagg tggaaatcaa acgaac 26

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide

<400> 55

aagcttctaa cactctcccc tgttg

25

<210> 56

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 56

aagcttatgg aatggatctg gatctttctc ctcatcctgt caggaactcg aggtgtccag 60
tcccagggtc agctggtg 78

<210> 57

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 57

ctgtaaggct tctggataca cattcactgc ctatgttata agctgggtga ggcaggcacc 60
tggacagggc ctg 74

<210> 58

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 58

ggtagtagtt attataatga gaagttcaag ggcagggtca caatgactag agacacatcc 60
accagcacag 70

<210> 59

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 59

gaggacactg cggtctatta ctgtgcaaga tccggggacg gcagtcggtt tgtttactgg 60
ggccaaggga cactagt 77

<210> 60

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 60

gtgtatccag aagccttaca ggacaccttc actgaagccc caggcttctt cacttcagct 60
ccagactgca ccagctgaac ctgggactgg 90

<210> 61

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 61

cttctcatta taataactac taccgcttcc aggataaatc tctcccatcc actcaaggcc 60
ctgtccaggt gcctgcc 77

<210> 62

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 62

gtaatagacc gcagtgtcct cagacctcag gctgctgagt tccatgtaga ctgtgctggt 60
ggatgtgtct c 71

<210> 63

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 63

gaattcatgg agacagacac aatcctgcta tgggtgctgc tgctctgggt tccaggctcc 60
actggtgac 69

<210> 64

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 64

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